



015936-2.ST25.txt
SEQUENCE LISTING

<110> SAHIN, ERINC
TARALP, ALPAY
SAYERS, SEHRA

<120> CIRCULAR RECOMBINANT PLASMID DNA CONSTRUCTS AND THEIR PROTEIN
PRODUCTS, METHODS OF PREPARATION AND IMMOBILISATION OF PROTEINS
ON SUPPORT

<130> U015936-2

<140> 10/550226
<141> 2005-09-20

<150> PCT/TR2003/000019
<151> 2003-03-20

<160> 13

<170> PatentIn version 3.3

<210> 1
<211> 733
<212> DNA
<213> Aequorea victoria

<220>
<221> gene
<222> (17)..(733)
<223> GFP gene

<400> 1
gggtaccggta gaaaaaatga gtaaaggaga agaacttttc actggagttg tcccaattct 60
tgttgaatta gatggtgatg ttaatgggca caaattttct gtcagtggag aggggtgaagg 120
tgatgcaaca tacggaaaac ttacccttaa atttatttgc actactggaa aactacctgt 180
tccatggcca acacttgtca ctactttctc ttatggtgtt caatgctttt cccgttatcc 240
ggatcatatg aaacggcatg actttttcaa gagtgccatg cccgaagggt atgtacagga 300
acgcactata tctttcaaag atgacgggaa ctacaagacg cgtgctgaag tcaagtttga 360
aggtgatacc cttgttaatc gtatcgagtt aaaagggtatt gatttttaaag aagatggaaa 420
cattctcgga caciaaactc agtacaacta taactcacac aatgtataca tcacggcaga 480
caaacaaaag aatggaatca aagctaactt caaaattcgc cacaacattg aagatggatc 540
cgttcaacta gcagaccatt atcaacaaaa tactccaatt ggcgatggcc ctgtcctttt 600
accagacaac cattacctgt cgacacaatc tgccctttcg aaagatccca acgaaaagcg 660
tgaccacatg gtccttcttg agtttgtaac tgctgctggg attacacatg gcatggatga 720
gctctacaaa taa 733

<210> 2
<211> 6029

<212> DNA
 <213> Artificial sequence

<220>
 <223> Empty PETM-11 plasmid

<220>
 <221> misc_feature
 <222> (1)..(6029)
 <223> Empty PETM-11 plasmid

<400> 2
 atccggatat agttcctcct ttcagcaaaa aaccctcaa gaccggttta gaggcccaa 60
 ggggttatgc tagttattgc tcagcggtag cagcagccaa ctacagcttc tttcgggctt 120
 tgtagcagc cggatctcag tggtagtggt ggtggtgctc gaggcggcc gcaagcttgt 180
 cgacggagct cgaattcggg tccggtacca ctatgtagag accaagacac gccttgtagc 240
 tgcctgcag ctttattctc ttgatgctgg tgctggaata gccctcatca ctgccgaggc 300
 tctgcatgct gccccgctcg tcagagtcgc tcacactgct gctgctccag tccagatcac 360
 ctgtgagata gtccgtgctc tccacgtcaa cgtcgatttc ttccctgtcg gaggcggagc 420
 gctccgagga gacggtaggag ccgatgctgt ccacccgat cctctcaatg cccagcttct 480
 ccagctgcct cttcaggtgt cgctgctctc gctgaagctg gtcgatttgg tgaacggctt 540
 ttctgtcaca atcttcaagt ttctttatgt gcaatttggc ttttgtaaat aaactcaacg 600
 tagtgtgtcg acttgattcg ggtcccagtg gcaccagccc cttcaacttc tccaggcaca 660
 agcgaagatg agcccgtcta ttcttctcca ttctattgtg agttgatctg ctactgctgt 720
 tattcttttt ggatttggtc ctccgtttta aggcattctt gtccttgttt ttgtatggtg 780
 acatggaggc ataaccatgt tcagcttctc tctcccgcg ctccagatag tcggccgcct 840
 ccagcagcat ctggatgttc atccgaaccg ccgcccgcct ggcgccctga aaataaagat 900
 tctcagtagt ggggatgtcg taatcgctca tggggtgatg gtgatggtga tgtttcatgg 960
 tatactctct tcttaaagtt aaatcaaaat tttttctaga ggggaattgt tatccgctca 1020
 caattccctt atagttagtc gtattaattt cgcgggatcg agatctcgat cctctacgcc 1080
 ggacgcatcg tggccggcat caccggcgcc acaggtgctg ttgctggcgc ctatatcgcc 1140
 gacatcaccg atggggaaga tcgggctcgc cacttcgggc tcatgagcgc ttgtttcggc 1200
 gtgggtatgg tggcaggccc cgtggccggg ggactgttgg gcgccatctc cttgcatgca 1260
 ccattccttg cggcggcggt gctcaacggc ctcaacctac tactgggctg cttcctaattg 1320
 caggagtcgc ataagggaga gcgtcgagat cccggacacc atcgaatggc gcaaaacctt 1380
 tcgcggtatg gcatgatagc gcccggaaga gaggcaattc aggggtggtga atgtgaaacc 1440
 agtaacgtta tacgatgtcg cagagtatgc cgggtgtctt tatcagaccg tttcccgctg 1500

015936-2.ST25.txt

ggtgaaccag gccagccacg tttctgcgaa aacgcgggaa aaagtggaag cggcgatggc 1560
 ggagctgaat tacattccca accgcgtggc acaacaactg gcgggcaaac agtcgttgct 1620
 gattggcggt gccacctcca gtctggccct gcacgcgccg tcgcaaattg tcgcggcgat 1680
 taaatctcgc gccgatcaac tgggtgccag cgtgggtggg tcgatggtag aacgaagcgg 1740
 cgtcgaagcc tgtaaagcgg cgggtgcaca tcttctcgcg caacgcgtca gtgggctgat 1800
 cattaactat ccgctggatg accaggatgc cattgctgtg gaagctgcct gcactaatgt 1860
 tccggcggtta tttcttgatg tctctgacca gacacccatc aacagtatta ttttctccca 1920
 tgaagacggt acgcgactgg gcgtggagca tctggctgca ttgggtcacc agcaaatcgc 1980
 gctgttagcg ggccattaa gttctgtctc ggcgcgctctg cgtctggctg gctggcataa 2040
 atatctcact cgcaatcaaa ttcagccgat agcggaaacgg gaaggcgact ggagtgccat 2100
 gtccggtttt caacaaacca tgcaaagtct gaatgagggc atcgttccca ctgcgatgct 2160
 ggttgccaac gatcagatgg cgctggggcg aatgcgcgcc attaccgagt ccgggctgcg 2220
 cgttgggtgc gatatctcgg tagtgggata cgacgatacc gaagacagct catgttatat 2280
 cccgccgtta accaccatca aacaggattt tcgcctgctg gggcaaacca gcgtggaccg 2340
 cttgctgcaa ctctctcagg gccaggcggt gaagggcaat cagctgttgc ccgtctcact 2400
 ggtgaaaaga aaaaccaccc tggcgcccaa tacgcaaacc gcctctcccc gcgcgttggc 2460
 cgattcatta atgcagctgg cacgacaggt ttcccactg gaaagcgggc agtgagcgca 2520
 acgaattaa tgtaagttag ctactcatt aggcaccggg atctcgaccg atgcccttga 2580
 gagccttcaa cccagtcagc tccttccggt gggcgcgggg catgactatc gtcgccgcac 2640
 ttatgactgt cttctttatc atgcaactcg taggacaggt gccggcagcg ctctgggtca 2700
 ttttcggcga ggaccgcttt cgctggagcg cgacgatgat cggcctgtcg cttgcggtat 2760
 tcggaatctt gcacgccctc gctcaagcct tcgtcactgg tcccgccacc aaacgtttcg 2820
 gcgagaagca ggccattatc gccggcatgg cggccccacg ggtgcgcatg atcgtgctcc 2880
 tgtcgttagg gacccggcta ggctggcggg gttgccttac tggttagcag aatgaatcac 2940
 cgatacgca gcgaacgtga agcgactgct gctgcaaaac gtctgcgacc tgagcaacaa 3000
 catgaatggt cttcggtttc cgtgtttcgt aaagtctgga aacgcggaag tcagcgccct 3060
 gcaccattat gttccggatc tgcacgcag gatgctgctg gctaccctgt ggaacaccta 3120
 catctgtatt aacgaagcgc tggcattgac cctgagtgat ttttctctgg tcccgccgca 3180
 tccataccgc cagttgttta ccctcacaac gttccagtaa ccgggcatgt tcatcatcag 3240
 taaccggtat cgtgagcatc ctctctcgtt tcacgggtat cattaccccc atgaacagaa 3300
 atccccctta cacggaggca tcagtgaaca aacaggaaaa aaccgccctt aacatggccc 3360
 gctttatcag aagccagaca ttaacgcttc tggagaaact caacgagctg gacgcggatg 3420

015936-2.ST25.txt

aacaggcaga	catctgtgaa	tcgcttcacg	accacgctga	tgagctttac	cgcagctgcc	3480
tcgcgcggtt	cggatgatgac	ggtgaaaacc	tctgacacat	gcagctcccc	gagacgggtca	3540
cagcttgtct	gtaagcggat	gccggggagca	gacaagcccc	tcagggcgcg	tcagcgggtg	3600
ttggcgggtg	tcggggcgca	gccatgaccc	agtcacgtag	cgatagcgga	gtgtatactg	3660
gcttaactat	gcggcatcag	agcagattgt	actgagagt	caccatatat	gcggtgtgaa	3720
ataccgcaca	gatgcgtaag	gagaaaatac	cgcacagggc	gctcttccgc	ttcctcgctc	3780
actgactcgc	tgcgctcgg	cgttcggctg	cggcgagcgg	tatcagctca	ctcaaaggcg	3840
gtaatacgg	tatccacaga	atcaggggat	aacgcaggaa	agaacatgtg	agcaaaaggc	3900
cagcaaaagg	ccaggaaccg	taaaaaggcc	gcgttgctgg	cgtttttcca	taggctccgc	3960
ccccctgacg	agcatcaca	aaatcgacgc	tcaagtcaga	ggtggcgaaa	cccgacagga	4020
ctataaagat	accaggcggt	tccccctgga	agctccctcg	tgcgctctcc	tgttccgacc	4080
ctgccgctta	ccggatacct	gtccgccttt	ctcccttcgg	gaagcgtggc	gctttctcat	4140
agctcacgct	gtaggtatct	cagttcgggtg	taggtcgttc	gctccaagct	gggctgtgtg	4200
cacgaacccc	ccgttcagcc	cgaccgctgc	gccttatccg	gtaactatcg	tcttgagtcc	4260
aacccggtaa	gacacgactt	atcgccactg	gcagcagcca	ctggtaacag	gattagcaga	4320
gcgaggtatg	taggcgggtg	tacagagttc	ttgaagtgg	ggcctaacta	cggctacact	4380
agaaggacag	tatttggtat	ctgcgctctg	ctgaagccag	ttaccttcgg	aaaaagagtt	4440
ggtagctctt	gatccggcaa	acaaaccacc	gctggtagcg	gtggtttttt	tgtttgcaag	4500
cagcagatta	cgcgcagaaa	aaaaggatct	caagaagatc	ctttgatctt	ttctacgggg	4560
tctgacgctc	agtggaaacga	aaactcacgt	taagggtatt	tggtcatgaa	caataaaact	4620
gtctgcttac	ataaacagta	atacaagggg	tgttatgagc	catattcaac	gggaaacgtc	4680
ttgctctagg	ccgcgattaa	attccaacat	ggatgctgat	ttatatgggt	ataaatgggc	4740
tcgcgataat	gtcgggcaat	caggtgcgac	aatctatcga	ttgtatggga	agcccgatgc	4800
gccagagtgt	tttctgaaac	atggcaaagg	tagcgttgcc	aatgatgtta	cagatgagat	4860
ggtcagacta	aactggctga	cggaaatttat	gcctcttccg	accatcaagc	attttatccg	4920
tactcctgat	gatgcatgg	tactcaccac	tgcatcccc	gggaaaacag	cattccaggt	4980
attagaagaa	tatcctgatt	caggtgaaaa	tattgttgat	gcgctggcag	tgttcctgcg	5040
ccggttgcat	tcgattcctg	tttgtaattg	tccttttaac	agcgatcgcg	tatttcgtct	5100
cgctcaggcg	caatcacgaa	tgaataacgg	tttggttgat	gcgagtgatt	ttgatgacga	5160
gcgtaatggc	tggcctgttg	aacaagtctg	gaaagaaatg	cataaacttt	tgccattctc	5220
accggattca	gtcgtcactc	atggtgattt	ctcacttgat	aaccttattt	ttgacgaggg	5280

015936-2.ST25.txt

gaaattaata ggttgatttg atgttggacg agtcggaatc gcagaccgat accaggatct 5340
 tgccatccta tggaactgcc tcggtgagtt ttctccttca ttacagaaac ggctttttca 5400
 aaaatatggt attgataatc ctgatatgaa taaattgcag tttcatttga tgctcgatga 5460
 gtttttctaa gaattaattc atgagcggat acatatttga atgtatttag aaaaataaac 5520
 aaataggggt tccgcgcaca tttccccgaa aagtgccacc tgaaattgta aacgttaata 5580
 ttttgtaaaa attcgcgtta aatttttgtt aaatcagctc attttttaac caataggccg 5640
 aaatcggcaa aatcccttat aaatcaaaag aatagaccga gatagggttg agtgttgttc 5700
 cagtttgtaa caagagtcca ctattaaaga acgtggactc caacgtcaaa gggcgaaaaa 5760
 ccgtctatca gggcgatggc ccactacgtg aaccatcacc ctaatcaagt tttttggggg 5820
 cgaggtgccg taaagcacta aatcgggaacc ctaaaggag ccccgattt agagcttgac 5880
 ggggaaagcc ggcgaacgtg gcgagaaagg aagggaagaa agcgaaagga gcgggcgcta 5940
 gggcgctggc aagtgtagcg gtcacgtgc gcgtaaccac cacaccgcc gcgcttaatg 6000
 cgccgctaca gggcgctcc cattcgcca 6029

<210> 3

<211> 5369

<212> DNA

<213> Artificial sequence

<220>

<223> Intermediate pETM-adp plasmid, on way to pETM-GFP-Imm construct

<400> 3

catcaccatc accatcacc catgagcgat tacgacatcc ccactactga gaatctttat 60
 tttcagggcg ccatgggagg cacggtaccg gatccgaatt cgagctccgt cgacaagctt 120
 gcggccgcac tcgagcacca ccaccaccac cactgagatc cggtctgctaa caaagcccga 180
 aaggaagctg agttggctgc tgccaccgct gagcaataac tagcataacc ccttggggcc 240
 tctaaacggg tcttgagggg ttttttgctg aaaggaggaa ctatatccgg attggcgaat 300
 gggacgcgcc ctgtagcggc gcattaagcg cggcgggtgt ggtggttacg cgcagcgtga 360
 ccgctacact tgccagcgcc ctagcgccc ctcctttcgc tttcttccct tcctttctcg 420
 ccacgttcgc cggctttccc cgtcaagctc taaatcgggg gctcccttta gggttccgat 480
 ttagtgcttt acggcacctc gaccccaaaa aacttgatta gggatgatgt tcacgtagtg 540
 ggccatcgcc ctgatagacg gtttttcgcc ctttgacgtt ggagtccacg ttctttaata 600
 gtggactctt gttccaaact ggaacaacac tcaaccctat ctcggtctat tcttttgatt 660
 tataagggat tttgccgatt tcggcctatt ggttaaaaaa tgagctgatt taacaaaaat 720
 ttaacgcgaa ttttaacaaa atattaacgt ttacaatttc aggtggcact tttcggggaa 780
 atgtgcgcgg aacccttatt tgtttatttt tctaaatata ttcaaataatg tatccgctca 840

015936-2.ST25.txt

tgaattaatt	cttagaaaaa	ctcatcgagc	atcaaatgaa	actgcaattt	attcatatca	900
ggattatcaa	taccatat	ttgaaaaagc	cgtttctgta	atgaaggaga	aaactcaccg	960
aggcagttcc	ataggatggc	aagatcctgg	tatcggtctg	cgattccgac	tcgtccaaca	1020
tcaatacaac	ctattaattt	cccctcgta	aaaataaggt	tatcaagtga	gaaatcacca	1080
tgagtgcga	ctgaatccgg	tgagaatggc	aaaagtttat	gcatttcttt	ccagacttgt	1140
tcaacaggcc	agccattacg	ctcgtcatca	aaatcactcg	catcaaccaa	accgttattc	1200
attcgtgatt	gcgcctgagc	gagacgaaat	acgcgatcgc	tgtaaaaagg	acaattacaa	1260
acaggaatcg	aatgcaaccg	gcgcaggaac	actgccagcg	catcaacaat	attttcacct	1320
gaatcaggat	attcttctaa	tacctggaat	gctgttttcc	cggggatcgc	agtggtagt	1380
aaccatgcat	catcaggagt	acggataaaa	tgcttgatgg	tcggaagagg	cataaattcc	1440
gtcagccagt	ttagtctgac	catctcatct	gtaacatcat	tggcaacgct	acctttgcca	1500
tgtttcagaa	acaactctgg	cgcatcgggc	ttcccataca	atcgatagat	tgtcgcacct	1560
gattgcccga	cattatcgcg	agcccattta	tacccatata	aatcagcatc	catgttgga	1620
tttaatcgcg	gcctagagca	agacgtttcc	cgttgaatat	ggctcataac	accccttgta	1680
ttactgttta	tgtaagcaga	cagttttatt	gttcatgacc	aaaatccctt	aacgtgagtt	1740
ttcgttccac	tgagcgtcag	accccgtaga	aaagatcaaa	ggatcttctt	gagatccttt	1800
ttttctgcgc	gtaatctgct	gcttgcaaac	aaaaaaacca	ccgctaccag	cggtgggttg	1860
tttgccggat	caagagctac	caactctttt	tccgaaggta	actggcttca	gcagagcgca	1920
gataccaaat	actgtccttc	tagtgtagcc	gtagttaggc	caccacttca	agaactctgt	1980
agcaccgcct	acatacctcg	ctctgcta	cctgttacca	gtggctgctg	ccagtggcga	2040
taagtcgtgt	cttaccgggt	tggactcaag	acgatagtta	ccggataagg	cgagcggtc	2100
gggctgaacg	gggggttcgt	gcacacagcc	cagcttgag	cgaacgacct	acaccgaact	2160
gagataccta	cagcgtgagc	tatgagaaa	cgccacgctt	cccgaaggga	gaaaggcgga	2220
caggtatccg	gtaagcggca	gggtcggaa	aggagagcgc	acgaggagc	ttccagggg	2280
aaacgcctgg	tatctttata	gtcctgtcgg	gtttcgccac	ctctgacttg	agcgtcgatt	2340
tttgtgatgc	tcgtcagggg	ggcggagcct	atggaaaaac	gccagcaacg	cggccttttt	2400
acgggttcctg	gccttttgct	ggccttttgc	tcacatgttc	tttcctgcgt	tatcccctga	2460
ttctgtggat	aaccgtatta	ccgcctttga	gtgagctgat	accgctcgcc	gcagccgaac	2520
gaccgagcgc	agcgagtcag	tgagcgagga	agcgggaagag	cgctgatgc	ggtattttct	2580
ccttacgcat	ctgtgcggta	tttcacaccg	catatatggt	gcactctcag	tacaatctgc	2640
tctgatgccg	catagttaag	ccagtataca	ctccgctatc	gctacgtgac	tgggtcatgg	2700

015936-2.ST25.txt

ctgcgccccg	acacccgcca	acacccgctg	acgcgcccctg	acgggcttgt	ctgctcccgg	2760
catccgctta	cagacaagct	gtgaccgtct	ccgggagctg	catgtgtcag	aggttttcac	2820
cgtcatcacc	gaaacgcgcg	aggcagctgc	ggtaaagctc	atcagcgtgg	tcgtgaagcg	2880
attcacagat	gtctgcctgt	tcatccgcgt	ccagctcgtt	gagtttctcc	agaagcgtta	2940
atgtctggct	tctgataaag	cgggccatgt	taagggcggt	tttttcctgt	ttggtcactg	3000
atgcctccgt	gtaaggggga	tttctgttca	tgggggtaat	gataccgatg	aaacgagaga	3060
ggatgctcac	gatacgggtt	actgatgatg	aacatgcccc	gttactggaa	cgttggtgagg	3120
gtaaacaact	ggcggtatgg	atgcggcggg	accagagaaa	aatcactcag	ggccaatgcc	3180
agcgcttcgt	taatacagat	gtaggtgttc	cacagggtag	ccagcagcat	cctgcgatgc	3240
agatccggaa	cataatgggtg	cagggcgctg	acttccgcgt	ttccagactt	tacgaaacac	3300
ggaaaccgaa	gaccattcat	gttgttgctc	aggctgcaga	cgttttgcag	cagcagtcgc	3360
ttcacgttcg	ctcgcgtatc	ggtgattcat	tctgctaacc	agtaaggcaa	ccccgccagc	3420
ctagccgggt	cctcaacgac	aggagcacga	tcatgcgcac	ccgtggggcc	gcatgccgg	3480
cgataatggc	ctgcttctcg	ccgaaacgtt	tgggtggcgg	accagtgcag	aaggcttgag	3540
cgagggcggtg	caagattccg	aataccgcaa	gcgacaggcc	gatcatcgtc	gcgctccagc	3600
gaaagcggtc	ctcgccgaaa	atgaccacga	gcgctgccgg	cacctgtcct	acgagttgca	3660
tgataaagaa	gacagtcata	agtgcggcga	cgatagtcac	gccccgcgcc	caccggaagg	3720
agctgactgg	gttgaagggt	ctcaagggca	tcggctcgaga	tcccgggtgcc	taatgagtga	3780
gctaacttac	attaattgctg	ttgcgctcac	tgccccgttt	ccagtcggga	aacctgtcgt	3840
gccagctgca	ttaatgaatc	ggccaacgcg	cggggagagg	cggtttgcgt	attggggcgcc	3900
aggggtggtt	ttctttttcac	cagtgcagacg	ggcaacagct	gattgccctt	caccgcctgg	3960
ccctgagaga	gttgcagcaa	gcgggtccacg	ctggtttgcc	ccagcaggcg	aaaatcctgt	4020
ttgatgggtg	ttaacggcgg	gatataacat	gagctgtctt	cggtatcgtc	gtatcccact	4080
accgagatat	ccgcaccaac	gcgcagcccc	gactcggtaa	tggcgcgcac	tgcgcccagc	4140
gccatctgat	cgttggcaac	cagcatcgca	gtgggaacga	tgccctcatt	cagcatttgc	4200
atggtttggt	gaaaaccgga	catggcactc	cagtcgcctt	cccgttccgc	tatcggtga	4260
atttgattgc	gagtgcagata	tttatgccag	ccagccagac	gcagacgcgc	cgagacagaa	4320
cttaatgggc	ccgctaacag	cgcgatttgc	tggtgacca	atgcgaccag	atgctccacg	4380
cccagtcgcg	taccgtcttc	atgggagaaa	ataatactgt	tgatgggtgt	ctggtcagag	4440
acatcaagaa	ataacgccgg	aacattagtg	caggcagctt	ccacagcaat	ggcatcctgg	4500
tcatccagcg	gatagttaat	gatcagccca	ctgacgcgtt	gcgcgagaag	attgtgcacc	4560
gccgctttac	aggcttcgac	gccgcttcgt	tctaccatcg	acaccaccac	gctggcaccc	4620

015936-2.ST25.txt

```

agttgatcgg cgcgagatTT aatcgccgCG acaatttgcg acggcgCGtg cagggccaga 4680
ctggagggtgg caacgccaat cagcaacgac tgtttgcccc ccagttgttg tgccacgcgg 4740
ttgggaatgt aattcagctc cgccatcgcc gcttccactt tttcccgcgt tttcgagaa 4800
acgtggctgg cctggttcac cacgcgggaa acggtctgat aagagacacc ggcatactct 4860
gcgacatcgt ataacgttac tggtttcaca ttcaccaccc tgaattgact ctcttccggg 4920
cgctatcatg ccataccgCG aaagggttttg cgccattcga tgggtgtccgg gatctcgacg 4980
ctctccctta tgcgactcct gcattaggaa gcagcccagt agtaggttga ggccgttgag 5040
caccgccgcc gcaaggaatg gtgcatgcaa ggagatggcg cccaacagtc ccccgccac 5100
ggggcctgcc accataccca cgccgaaaca agcgctcatg agcccgaagt ggcgagcccg 5160
atcttcccca tcggtgatgt cggcgatata ggcgccagca accgcacctg tggcgccggt 5220
gatgccggcc acgatgcgtc cggcgtagag gatcgagatc tcgatcccgC gaaattaata 5280
cgactcacta taggggaatt gtgagcggat aacaattccc ctctagaaat aattttgatt 5340
taactttaag aaggagatat accatgaaa 5369

```

<210> 4
 <211> 3337
 <212> DNA
 <213> Artificial sequence

<220>
 <223> pGFPuv plasmid coding for GFP from Aequorea victoria

<220>
 <221> CDS
 <222> (286)..(1014)
 <223> pGFPuv plasmid coding for GFP from Aequorea victoria

```

<400> 4
agcgccaat acgcaaaccg cctctccccg cgcgttgGCC gattcattaa tgcagctggc 60
acgacagggt tccccgactgg aaagcgggca gtgagcgcaa cgcaattaat gtgagttagc 120
tcactcatta ggcaccccag gctttacact ttatgcttcc ggctcgtatg ttgtgtggaa 180
ttgtgagcgg ataacaattt cacacaggaa acagctatga ccatgattac gccaagcttg 240
catgcctgca ggtcgactct agaggatccc cgggtaccgg tagaa aaa atg agt aaa 297
                                Lys Met Ser Lys
                                1

```

```

gga gaa gaa ctt ttc act gga gtt gtc cca att ctt gtt gaa tta gat 345
Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
5          10          15          20
ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag ggt gaa ggt 393
Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
25          30          35

```


015936-2.ST25.txt

gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc act act gga Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly	441
aaa cta cct gtt cca tgg cca aca ctt gtc act act ttc tct tat ggt Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly	489
gtt caa tgc ttt tcc cgt tat ccg gat cat atg aaa cgg cat gac ttt Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe	537
ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa cgc act ata tct Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Ser	585
ttc aaa gat gac ggg aac tac aag acg cgt gct gaa gtc aag ttt gaa Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu	633
ggt gat acc ctt gtt aat cgt atc gag tta aaa ggt att gat ttt aaa Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys	681
gaa gat gga aac att ctc gga cac aaa ctc gag tac aac tat aac tca Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser	729
cac aat gta tac atc acg gca gac aaa caa aag aat gga atc aaa gct His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala	777
aac ttc aaa att cgc cac aac att gaa gat gga tcc gtt caa cta gca Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala	825
gac cat tat caa caa aat act cca att ggc gat ggc cct gtc ctt tta Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu	873
cca gac aac cat tac ctg tcg aca caa tct gcc ctt tcg aaa gat ccc Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro	921
aac gaa aag cgt gac cac atg gtc ctt ctt gag ttt gta act gct gct Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala	969
ggg att aca cat ggc atg gat gag ctc tac aaa taa tga att cca Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ile Pro	1014
actgagcgcc ggtagctacc attaccaact tgtctggtgt caaaaataat aggcctacta	1074
gtcggccgta cgggcccttt cgtctcgcgc gtttcggtga tgacggtgaa aacctctgac	1134
acatgcagct cccggagacg gtcacagctt gtctgtaagc ggatgccggg agcagacaag	1194
cccgctcaggg cgcgtcagcg ggtgttggtg ggtgtcgggg ctggcttaac tatgcggcat	1254
cagagcagat tgtactgaga gtgcaccata tgcggtgtga aataccgcac agatgcgtaa	1314
ggagaaaata ccgcatcagg cggccttaag ggcctcgtga tacgcctatt tttatagggt	1374

015936-2.ST25.txt

aatgtcatga	taataatggt	ttcttagacg	tcaggtggca	cttttcgggg	aatgtg'gc	1434
ggaacccta	tttgtttatt	tttctaaata	cattcaaata	tgtatccgct	catgagacaa	1494
taaccctgat	aaatgcttca	ataatattga	aaaaggaaga	gtatgagtat	tcaacatttc	1554
cgtgtcggc	ttattccctt	ttttgcggca	ttttgccttc	ctgtttttgc	tcaccagaa	1614
acgctggtga	aagtaaaaga	tgctgaagat	cagttgggtg	cacgagtggg	ttacatcgaa	1674
ctggatctca	acagcggtaa	gaccttgag	agttttcgcc	ccgaagaacg	ttttccaatg	1734
atgagcactt	ttaaagttct	gctatgtggc	gcggtattat	cccgtattga	cgccgggcaa	1794
gagcaactcg	gtcggccgat	acactattct	cagaatgact	tggttgagta	ctcaccagtc	1854
acagaaaagc	atcttacgga	tggcatgaca	gtaagagaat	tatgcagtgc	tgccataacc	1914
atgagtgata	acactgcggc	caacttactt	ctgacaacga	tcggaggacc	gaaggagcta	1974
accgcttttt	tgcacaacat	gggggatcat	gtaactcgcc	ttgatcgttg	ggaaccggag	2034
ctgaatgaag	ccataccaaa	cgacgagcgt	gacaccacga	tgctgtagc	aatggcaaca	2094
acgttgcgca	aactattaac	tggcgaaacta	cttactctag	cttcccggca	acaattaata	2154
gactggatgg	aggcggataa	agttgcagga	ccacttctgc	gctcggccct	tccggctggc	2214
tggtttattg	ctgataaatc	tggagccggt	gagcgtgggt	ctcgcggtat	cattgcagca	2274
ctggggccag	atggtaagcc	ctcccgtatc	gtagttatct	acacgacggg	gagtcaggca	2334
actatggatg	aacgaaatag	acagatcgct	gagatagggtg	cctcactgat	taagcattgg	2394
taactgtcag	accaagttta	ctcatatata	ctttagattg	atttaaaact	tcatttttaa	2454
tttaaaagga	tctaggtgaa	gatccttttt	gataatctca	tgaccaaact	cccttaacgt	2514
gagttttcgt	tccactgagc	gtcagacccc	gtagaaaaga	tcaaaggatc	ttcttgagat	2574
cctttttttc	tgcgcgtaat	ctgctgcttg	caaacaaaaa	aaccaccgct	accagcgggtg	2634
gtttgtttgc	cggatcaaga	gctaccaact	ctttttccga	aggtaactgg	cttcagcaga	2694
gcgcagatac	caaatactgt	ccttctagt	tagccgtagt	taggccacca	cttcaagaac	2754
tctgtagcac	cgcctacata	cctcgtcttg	ctaactcctgt	taccagtggc	tgctgccagt	2814
ggcgataagt	cgtgtcttac	cgggttggac	tcaagacgat	agttaccgga	taaggcgcag	2874
cggtcgggct	gaacgggggg	ttcgtgcaca	cagcccagct	tgagcgaac	gacctacacc	2934
gaactgagat	acctacagcg	tgagctatga	gaaagcgcca	cgcttcccga	agggagaaaag	2994
gcggacaggt	atccggttaag	cggcagggtc	ggaacaggag	agcgcacgag	ggagcttcca	3054
gggggaaacg	cctggatatct	ttatagtcct	gtcgggtttc	gccacctctg	acttgagcgt	3114
cgatttttgt	gatgtctgtc	agggggggcg	agcctatgga	aaaacgccag	caacgcggcc	3174
tttttacggt	tcctggcctt	ttgctggcct	tttgctcaca	tgttctttcc	tgcgttatcc	3234

cctgattctg tggataaccg tattaccgcc tttagtgag ctgataccgc tcgccgcagc 3294

cgaacgaccg agcgcagcga gtcagtgagc gaggaagcgg aag 3337

<210> 5

<211> 239

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic Construct

<400> 5

Lys Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

015936-2.ST25.txt

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 6

<211> 6069

<212> DNA

<213> Artificial sequence

<220>

<223> pETM-GFP-Imm plasmid containing Hisx6 tag, flexible joint
as frame adapter, and A. victoria GFP gene

<220>

<221> CDS

<222> (1)..(876)

<223> pETM-GFP-Imm plasmid containing Hisx6 tag, flexible joint
as frame adapter, and A. victoria GFP gene

<400> 6

atg aaa cat cac cat cac cat cac ccc atg agc gat tac gac atc ccc 48
Met Lys His His His His His Pro Met Ser Asp Tyr Asp Ile Pro
1 5 10 15

act act gag aat ctt tat ttt cag ggc gcc atg gga ggc acg gta ccg 96
Thr Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Gly Gly Thr Val Pro
20 25 30

gta gaa aaa atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca 144
Val Glu Lys Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
35 40 45

att ctt gtt gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc 192
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
50 55 60

agt gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa 240
Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
65 70 75 80

ttt att tgc act act gga aaa cta cct gtt cca tgg cca aca ctt gtc 288
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
85 90 95

act act ttc tct tat ggt gtt caa tgc ttt tcc cgt tat ccg gat cat 336
Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
100 105 110

atg aaa cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta 384
Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
115 120 125

015936-2.ST25.txt

cag gaa cgc act ata tct ttc aaa gat gac ggg aac tac aag acg cgt Gln Glu Arg Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg 130 135 140	432
gct gaa gtc aag ttt gaa ggt gat acc ctt gtt aat cgt atc gag tta Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu 145 150 155 160	480
aaa ggt att gat ttt aaa gaa gat gga aac att ctc gga cac aaa ctc Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu 165 170 175	528
gag tac aac tat aac tca cac aat gta tac atc acg gca gac aaa caa Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln 180 185 190	576
aag aat gga atc aaa gct aac ttc aaa att cgc cac aac att gaa gat Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp 195 200 205	624
gga tcc gtt caa cta gca gac cat tat caa caa aat act cca att ggc Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly 210 215 220	672
gat ggc cct gtc ctt tta cca gac aac cat tac ctg tcg aca caa tct Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser 225 230 235 240	720
gcc ctt tcg aaa gat ccc aac gaa aag cgt gac cac atg gtc ctt ctt Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu 245 250 255	768
gag ttt gta act gct gct ggg att aca cat ggc atg gat gag ctc cgt Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Arg 260 265 270	816
cga caa gct tgc ggc cgc act cga gca cca cca cca cca cca ctg aga Arg Gln Ala Cys Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg 275 280 285	864
tcc ggc tgc taa caaagcccga aaggaagctg agttggctgc tgccaccgct Ser Gly Cys 290	916
gagcaataac tagcataacc ccttggggcc tctaaacggg tcttgagggg ttttttgctg 976	
aaaggaggaa ctatatccgg attggcgaat gggacgcgcc ctgtagcggc gcattaagcg 1036	
cggcggggtgt ggtggttacg cgcagcgtga ccgctacact tgccagcgcc ctagcgcgccg 1096	
ctcctttcgc tttcttcctt tcctttctcg ccacgttcgc cggctttccc cgtcaagctc 1156	
taaatcgggg gctcccttta gggttccgat ttagtgcttt acggcacctc gaccccaaaa 1216	
aacttgatta gggatgatggg tcacgtagtg ggccatcgcc ctgatagacg gtttttcgcc 1276	
ctttgacgtt ggagtccacg ttctttaata gtggactctt gttccaaact ggaacaacac 1336	
tcaaccctat ctcggtctat tcttttgatt tataagggat tttgccgatt tcggcctatt 1396	
ggttaaaaaa tgagctgatt taacaaaaat ttaacgcgaa ttttaacaaa atattaacgt 1456	
ttacaatttc aggtggcact tttcggggaa atgtgcgcgg aacccttatt tgtttttttt 1516	

015936-2.ST25.txt

tctaaataca	ttcaaatatg	tatccgctca	tgaattaatt	cttagaaaaa	ctcatcgagc	1576
atcaaataaa	actgcaatgt	attcatatca	ggattatcaa	taccatattt	ttgaaaaagc	1636
cgtttctgta	atgaaggaga	aaactcaccg	aggcagttcc	ataggatggc	aagatcctgg	1696
tatcgggtctg	cgattccgac	tcgtccaaca	tcaatacaac	ctattaattt	cccctcgtca	1756
aaaataaggt	tatcaagtga	gaaatcacca	tgagtgcgca	ctgaatccgg	tgagaatggc	1816
aaaagtttat	gcatttcttt	ccagacttgt	tcaacaggcc	agccattacg	ctcgtcatca	1876
aaatcactcg	catcaaccaa	accgttattc	attcgtgatt	gcgcctgagc	gagacgaaat	1936
acgcgatcgc	tgtaaaaagg	acaattacaa	acaggaatcg	aatgcaaccg	gcgcaggaac	1996
actgccagcg	catcaacaat	attttcacct	gaatcaggat	attcttctaa	tacctggaat	2056
gctgttttcc	cggggatcgc	agtggtgagt	aaccatgcat	catcaggagt	acggataaaa	2116
tgcttgatgg	tcggaagagg	cataaattcc	gtcagccagt	ttagtctgac	catctcatct	2176
gtaacatcat	tggcaacgct	acctttgcc	tgtttcagaa	acaactctgg	cgcacgggc	2236
ttcccataca	atcgatagat	tgtcgcacct	gattgcccga	cattatcgcg	agcccattta	2296
tacccatata	aatcagcatc	catgttgga	tttaatcgcg	gcctagagca	agacgtttcc	2356
cgttgaatat	ggctcataac	acccttgta	ttactgttta	tgtaagcaga	cagttttatt	2416
gttcatgacc	aaaatccctt	aacgtgagtt	ttcgttccac	tgagcgtcag	accccgtaga	2476
aaagatcaaa	ggatcttctt	gagatccttt	ttttctgctc	gtaatctgct	gcttgcaaac	2536
aaaaaaacca	ccgctaccag	cggtggtttg	tttgccggat	caagagctac	caactctttt	2596
tccgaaggta	actggcttca	gcagagcgca	gataccaaat	actgtccttc	tagtgtagcc	2656
gtagttaggc	caccacttca	agaactctgt	agcaccgcct	acatacctcg	ctctgcta	2716
cctgttacca	gtggctgctg	ccagtggcga	taagtctgtg	cttaccgggt	tggactcaag	2776
acgatagtta	ccggataagg	cgagcggtc	gggctgaacg	gggggttcgt	gcacacagcc	2836
cagcttgag	cgaacgacct	acaccgaact	gagataccta	cagcgtgagc	tatgagaaag	2896
cgccacgctt	cccgaaggga	gaaaggcgga	caggtatccg	gtaagcgga	gggtcggaac	2956
aggagagcgc	acgagggagc	ttccaggggg	aaacgcctgg	tatctttata	gtcctgtcgg	3016
gtttcgccac	ctctgacttg	agcgtcgatt	tttgtgatgc	tcgtcagggg	ggcggagcct	3076
atggaaaaac	gccagcaacg	cggccttttt	acggttctctg	gccttttgct	ggccttttgc	3136
tcacatgttc	tttcctgctg	tatcccctga	ttctgtggat	aaccgtatta	ccgcctttga	3196
gtgagctgat	accgctcgcc	gcagccgaac	gaccgagcgc	agcgagtcag	tgagcgagga	3256
agcggaagag	cgctgatgc	ggtattttct	ccttacgcat	ctgtgcggta	tttcacaccg	3316
catatatggt	gcactctcag	tacaatctgc	tctgatgccg	catagttaag	ccagtataca	3376

015936-2.ST25.txt

ctccgctatc gctacgtgac tgggtcatgg ctgcgccccg acacccgcca acacccgctg	3436
acgcgccctg acgggcttgt ctgctccccg catccgctta cagacaagct gtgaccgtct	3496
ccgggagctg catgtgtcag aggttttcac cgtcatcacc gaaacgcgcg aggcagctgc	3556
ggtaaagctc atcagcgtgg tcgtgaagcg attcacagat gtctgcctgt tcatccgcgt	3616
ccagctcgtt gagtttctcc agaagcgta atgtctggct tctgataaag cgggccatgt	3676
taagggcggt ttttctctgt ttggctactg atgcctccgt gtaaggggga tttctgttca	3736
tgggggtaat gataccgatg aaacgagaga ggatgctcac gatacgggtt actgatgatg	3796
aacatgcccc gttactggaa cgttgtgagg gtaaacaact ggcggtatgg atgcggcggg	3856
accagagaaa aatcactcag ggtcaatgcc agcgcttcgt taatacagat gtaggtgttc	3916
cacagggtag ccagcagcat cctgcgatgc agatccggaa cataatggtg cagggcgctg	3976
acttccgcgt ttccagactt tacgaaacac ggaaaccgaa gaccattcat gttgttgctc	4036
aggtcgcaga cgttttgcag cagcagtcgc ttacagttcg ctgcgctatc ggtgattcat	4096
tctgctaacc agtaaggcaa ccccgccagc ctagccgggt cctcaacgac aggagcacga	4156
tcatgcgcac ccgtggggcc gccatgccgg cgataatggc ctgcttctcg ccgaaacgtt	4216
tgggtggcggg accagtgcag aaggcttgag cgagggcgctg caagattccg aataccgcaa	4276
gcgacaggcc gatcatcgtc gcgctccagc gaaagcggtc ctgcgccgaa atgaccaga	4336
gcgctgccgg cacctgtcct acgagttgca tgataaagaa gacagtcata agtgcggcga	4396
cgatagtcat gccccgcgcc caccggaagg agctgactgg gttgaaggct ctcaagggca	4456
tcggtcgaga tcccggtgcc taatgagtga gctaacttac attaatgctg ttgcgctcac	4516
tgcccgtttt ccagtcggga aacctgtcgt gccagctgca ttaatgaatc ggccaacgcg	4576
cggggagagg cggtttgcgt attgggcgcc aggggtggtt ttttttcac cagtgcagcg	4636
ggcaacagct gattgccctt caccgcctgg ccctgagaga gttgcagcaa gcggtccacg	4696
ctggtttgcc ccagcaggcg aaaatcctgt ttgatggtgg ttaacggcgg gatataacat	4756
gagctgtctt cggtatcgtc gtatcccact accgagatat ccgcaccaac gcgcagcccg	4816
gactcggtaa tggcgcgcat tgcgcccagc gccatctgat cgttggcaac cagcatcgca	4876
gtgggaacga tgccctcatt cagcatttgc atggtttgtt gaaaaccgga catggcactc	4936
cagtcgcctt cccgttccgc tatcggtga atttgattgc gagtgcagata tttatgccag	4996
ccagccagac gcagacgcgc cgagacagaa cttaatgggc ccgctaacag cgcgatttgc	5056
tggtgacca atgcgaccag atgctccacg cccagtcgcg taccgtcttc atgggagaaa	5116
ataatactgt tgatgggtgt ctggtcagag acatcaagaa ataacgccgg aacattagt	5176
caggcagctt ccacagcaat ggcacacctg tcatccagcg gatagttaat gatcagccca	5236
ctgacgcgtt gcgcgagaag attgtgcacc gccgctttac aggccttcgac gccgcttcgt	5296

015936-2.ST25.txt

```
tctaccatcg acaccaccac gctggcacc agttgatcgg cgcgagattt aatcgccgcg 5356
acaatttgcg acggcgcggtg cagggccaga ctggaggttg caacgccaat cagcaacgac 5416
tgtttgcccg ccagttgttg tgccacgcgg ttgggaatgt aattcagctc cgccatcgcc 5476
gcttccactt tttcccgcg tttcgcagaa acgtggctgg cctggttcac cacgcgggaa 5536
acgggtctgat aagagacacc ggcatactct gcgacatcgt ataacgttac tggtttcaca 5596
ttcaccaccc tgaattgact ctcttcggg cgctatcatg ccataccgcg aaagggtttg 5656
cgccattcga tgggtgccg gatctcgacg ctctccctta tgcgactcct gcattaggaa 5716
gcagcccagt agtaggttga ggccgttgag caccgccgcc gcaaggaatg gtgcatgcaa 5776
ggagatggcg cccaacagtc ccccgccac ggggcctgcc accatacca cgccgaaaca 5836
agcgctcatg agcccgaagt ggcgagcccg atcttcccca tcggtgatgt cggcgatata 5896
ggcgccagca accgcacctg tggcgccggt gatgccggcc acgatgcgtc cggcgtagag 5956
gatcgagatc tcgatccgc gaaattaata cgactcacta taggggaatt gtgagcggat 6016
aacaattccc ctctagaaat aattttgatt taactttaag aaggagatat acc 6069
```

<210> 7
 <211> 291
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic Construct

<400> 7

Met Lys His His His His His Pro Met Ser Asp Tyr Asp Ile Pro
 1 5 10 15

Thr Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Gly Gly Thr Val Pro
 20 25 30

Val Glu Lys Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 35 40 45

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
 50 55 60

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 65 70 75 80

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
 85 90 95

Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
 Page 16

015936-2.ST25.txt
100 105 110

Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
115 120 125

Gln Glu Arg Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
130 135 140

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
145 150 155 160

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
165 170 175

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
180 185 190

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
195 200 205

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
210 215 220

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
225 230 235 240

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
245 250 255

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Arg
260 265 270

Arg Gln Ala Cys Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg
275 280 285

Ser Gly Cys
290

<210> 8
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> Frame adapter used for prevention of frameshift mutation as a
result of plasmid modification

<220>

<221> misc_feature
 <222> (1)..(17)
 <223> Frame adapter used for prevention of frameshift mutation as a
 result of plasmid modification

<400> 8
 catgggaggc acgtac

17

<210> 9
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide design based on size and flexibility to act as a linker
 between the tag and GFP protein segments

<220>
 <221> MISC_FEATURE
 <223> Peptide design based on size and flexibility to act as a linker
 between the tag and GFP protein segments

<400> 9

Met Gly Gly Thr Val
 1 5

<210> 10
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide design based on charge and shape to bind the
 expressed protein to a suitably interactive surface

<220>
 <221> MISC_FEATURE
 <223> Peptide design based on charge and shape to bind the
 expressed protein to a suitably interactive surface

<400> 10

His His His His His His
 1 5

<210> 11
 <211> 238
 <212> PRT
 <213> Aequorea victoria

<220>
 <221> MISC_FEATURE
 <223> Green fluorescent peptide coded by pGFPuv plasmid, permitting

015936-2.ST25.txt
easy visualisation and quantification based on fluorescence
properties

<400> 11

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 12
 <211> 291
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Completed peptide based on Hisx6 tag, short physically flexible linker and green fluorescent protein coded by pETM-GFP-Imm to impart fluorescence properties, allowing easy immobilisation with retention of bioactivity, visualisation and quantification

<220>
 <221> MISC_FEATURE
 <223> Completed peptide based on Hisx6 tag, short physically flexible linker and green fluorescent protein coded by pETM-GFP-Imm to impart fluorescence properties, allowing easy immobilisation with retention of bioactivity, visualisation and quantification

<400> 12

Met Lys His His His His His His Pro Met Ser Asp Tyr Asp Ile Pro
 1 5 10 15

Thr Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Gly Gly Thr Val Pro
 20 25 30

Val Glu Lys Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 35 40 45

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
 50 55 60

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 65 70 75 80

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
 85 90 95

Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
 100 105 110

Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
 115 120 125

Gln Glu Arg Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
 130 135 140

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
 145 150 155 160

015936-2.ST25.txt

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
165 170 175

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
180 185 190

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
195 200 205

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
210 215 220

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
225 230 235 240

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
245 250 255

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Arg
260 265 270

Arg Gln Ala Cys Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg
275 280 285

Ser Gly Cys
290

<210> 13

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Frame adapter

<400> 13

gtacgccatg ggaggcacgg taccttgtg

29